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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=2; hr=14; min=49; sec=27; ms=527; ]

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Application No: 10558627 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2007-11-14 09:19:11.293  
**Finished:** 2007-11-14 09:19:12.820  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 527 ms  
**Total Warnings:** 18  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 21  
**Actual SeqID Count:** 21

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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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<120> GLP-1 Analog Fusion Proteins  
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<141> 2005-11-29  
<150> 60/477880  
<151> 2003-06-12  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly Gly  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Gly  
20 25 30

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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly Pro  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Pro  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly  
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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly  
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20 25 30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
35 40 45

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Xaa  
65 70 75 80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
85 90 95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
100 105 110

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
115 120 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn  
130 135 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
145 150 155 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg  
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys  
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
210 215 220

Ser Leu Ser Leu Gly Xaa  
225 230

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<400> 9

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly  
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly  
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His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu  
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Gly  
20 25 30

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
35 40 45

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ala Glu Ser  
50 55 60

Lys Tyr Gly Pro Pro Cys Pro  
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Trp Leu Val Lys Gly Gly Gly

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Trp Leu Lys Asn Gly Gly Gly  
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Trp Leu Lys Asn Gly Gly Pro  
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Trp Leu Val Lys Gly Gly  
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Trp Leu Lys Asn Gly Gly  
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<400> 18

Pro Pro Cys Pro Ser Cys  
1 5

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<400> 19

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Ser Gly Gly Gly Gly Ser  
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tctgggtggcg gtggcagcgc tgagtccaaa tatggtcccc catgcccacc ctgcccagca 180

cctgaggccg ccgggggacc atcagtctc ctgttccccc caaaacccaa ggacactctc	240
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Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
20				25			30					